

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

1.-24. (Canceled).

25. (New) An RNA sequence analyzer comprising:

a grammar storage unit that stores a structural topology of RNA secondary structures with a grammar corresponding to the structural topology;

a parsing unit that derives parse trees by applying one or more RNA sequences to the one or more grammars;

a goodness-of-fit calculation unit that calculates goodnesses of fit of the parse trees derived by the parsing unit; and

an output unit that outputs the RNA sequences, from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived, as RNA sequence candidates that could potentially form the secondary structures consistent with the structural topology.

26. (New) The RNA sequence analyzer according to claim 25, further comprising:

a sorting unit that sorts the parse trees having the goodnesses of fit that satisfy preset conditions in a descending order of the goodnesses of fit, wherein the output unit outputs the parse trees sorted by the sorting unit as secondary structure candidates of the RNA sequence.

27. (New) The RNA sequence analyzer according to claim 25, further comprising:

an extraction unit that extracts the RNA sequences from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived; and

a common structure matrix creation unit that displays the structural topologies and the RNA sequences in a two-dimensional matrix, that gives marks to lattice parts corresponding to the RNA sequences extracted by the extraction unit and the structural topologies in the two-dimensional matrix, and that thereby visualizes the structural topologies common to the RNA sequences.

28. (New) The RNA sequence analyzer according to claim 25, further comprising:
an RNA sequence production unit that produces RNA sequences transcribed from a DNA sequence input by a user; and
a gene prediction unit that predicts parts of the DNA sequence corresponding to the RNA sequences, from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived, as gene candidates,
wherein the parsing unit derives the parse trees by applying the one or more grammars to the RNA sequences produced by the RNA sequence production unit.
29. (New) The RNA sequence analyzer according to claim 25, further comprising:
a similarity calculation unit that calculates a similarity among the RNA sequences based on the goodnesses of fit calculated by the goodness-of-fit calculation unit.
30. (New) The RNA sequence analyzer according to claim 25, further comprising:
an extraction unit that extracts the RNA sequences from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived;
a goodness-of-fit matrix creation unit that creates a goodness-of-fit matrix which displays the structural topologies and the RNA sequences in a two-dimensional matrix, and which displays the goodnesses of fit on lattice parts corresponding to the RNA sequences extracted by the extraction unit and the structural topologies in the two-dimensional matrix; and
a common structure extraction unit that sorts the structural topologies according to the goodnesses of fit for the goodness-of-fit matrix created by the goodness-of-fit matrix creation unit, that parses other RNA sequences based on the grammar corresponding to an order of the sorted structural topologies, and obtains the parse trees having optimum goodnesses of fit, and that extracts the other RNA sequences corresponding to the parse trees having the goodnesses of fit that satisfy the preset conditions.

31. (New) An RNA sequence analysis method, comprising:

- a grammar storage step that stores a structural topology of RNA secondary structures with a grammar corresponding to the structural topology;
- a parsing step that derives parse trees by applying one or more RNA sequences to the one or more grammars;
- a goodness-of-fit calculation step that calculates goodnesses of fit of the parse trees derived by the parsing step; and
- an output step that outputs the RNA sequences, from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived, as RNA sequence candidates that could potentially form the secondary structures consistent with the structural topology.

32. (New) The RNA sequence analysis method according to claim 31, further comprising:

- a sorting step that sorts the parse trees having the goodnesses of fit that satisfy preset conditions in a descending order of the goodnesses of fit, wherein the output step outputs the parse trees sorted by the sorting step as secondary structure candidates of the RNA sequence.

33. (New) The RNA sequence analysis method according to claim 31, further comprising:

- an extraction step that extracts the RNA sequences from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived; and
- a common structure matrix creation step that displays the structural topologies and the RNA sequences in a two-dimensional matrix, that gives marks to lattice parts corresponding to the RNA sequences extracted by the extraction step and the structural topologies in the two-dimensional matrix, and that thereby visualizes the structural topologies common to the RNA sequences.

34. (New) The RNA sequence analysis method according to claim 31, further comprising:

- an RNA sequence production step that produces RNA sequences transcribed from a DNA sequence input by a user; and

a gene prediction step that predicts parts of the DNA sequence corresponding to the RNA sequences, from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived, as gene candidates,

wherein the parsing step derives the parse trees by applying the one or more grammars to the RNA sequences produced by the RNA sequence production step.

35. (New) The RNA sequence analysis method according to claim 31, further comprising:

a similarity calculation step that calculates a similarity among the RNA sequences based on the goodnesses of fit calculated by the goodness-of-fit calculation step.

36. (New) The RNA sequence analysis method according to claim 31, further comprising:

an extraction step that extracts the RNA sequences from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived;

a goodness-of-fit matrix creation step that creates a goodness-of-fit matrix which displays the structural topologies and the RNA sequences in a two-dimensional matrix, and which displays the goodnesses of fit on lattice parts corresponding to the RNA sequences extracted by the extraction step and the structural topologies in the two-dimensional matrix; and

a common structure extraction step that sorts the structural topologies according to the goodnesses of fit for the goodness-of-fit matrix created by the goodness-of-fit matrix creation step, that parses other RNA sequences based on the grammar corresponding to an order of the sorted structural topologies, and obtains the parse trees having optimum goodnesses of fit, and that extracts the other RNA sequences corresponding to the parse trees having the goodnesses of fit that satisfy the preset conditions.

37. (New) A computer program product, embodied in a computer readable medium, that makes a computer execute an RNA sequence analysis method, comprising:

a grammar storage step that stores a structural topology of RNA secondary structures with a grammar corresponding to the structural topology;

a parsing step that derives parse trees by applying one or more RNA sequences to the one or more grammars;

a goodness-of-fit calculation step that calculates goodnesses of fit of the parse trees derived by the parsing step; and

an output step that outputs the RNA sequences, from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived, as RNA sequence candidates that could potentially form the secondary structures consistent with the structural topology.

38. (New) The computer program product according to claim 37, further comprising:

a sorting step that sorts the parse trees having the goodnesses of fit that satisfy preset conditions in a descending order of the goodnesses of fit, wherein the output step outputs the parse trees sorted by the sorting step as secondary structure candidates of the RNA sequence.

39. (New) The computer program product according to claim 37, further comprising:

an extraction step that extracts the RNA sequences from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived; and

a common structure matrix creation step that displays the structural topologies and the RNA sequences in a two-dimensional matrix, that gives marks to lattice parts corresponding to the RNA sequences extracted by the extraction step and the structural topologies in the two-dimensional matrix, and that thereby visualizes the structural topologies common to the RNA sequences.

40. (New) The computer program product according to claim 37, further comprising:

an RNA sequence production step that produces RNA sequences transcribed from a DNA sequence input by a user; and

a gene prediction step that predicts parts of the DNA sequence corresponding to the RNA sequences, from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived, as gene candidates,

wherein the parsing step derives the parse trees by applying the one or more grammars to the RNA sequences produced by the RNA sequence production step.

41. (New) The computer program product according to claim 37, further comprising:

a similarity calculation step that calculates a similarity among the RNA sequences based on the goodnesses of fit calculated by the goodness-of-fit calculation step.

42. (New) The computer program product according to claim 37, further comprising:
an extraction step that extracts the RNA sequences from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived;

a goodness-of-fit matrix creation step that creates a goodness-of-fit matrix which displays the structural topologies and the RNA sequences in a two-dimensional matrix, and which displays the goodnesses of fit on lattice parts corresponding to the RNA sequences extracted by the extraction step and the structural topologies in the two-dimensional matrix;
and

a common structure extraction step that sorts the structural topologies according to the goodnesses of fit for the goodness-of-fit matrix created by the goodness-of-fit matrix creation step, that parses other RNA sequences based on the grammar corresponding to an order of the sorted structural topologies, and obtains the parse trees having optimum goodnesses of fit, and that extracts the other RNA sequences corresponding to the parse trees having the goodnesses of fit that satisfy the preset conditions.

43. (New) A computer readable recording medium storing a computer program that makes a computer execute an RNA sequence analysis method, comprising:

a grammar storage step that stores a structural topology of RNA secondary structures with a grammar corresponding to the structural topology;

a parsing step that derives parse trees by applying one or more RNA sequences to the one or more grammars;

a goodness-of-fit calculation step that calculates goodnesses of fit of the parse trees derived by the parsing step; and

an output step that outputs of the RNA sequences, from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived, as RNA sequence candidates that could potentially form the secondary structures consistent with the structural topology.

44. (New) The computer readable recording medium according to claim 43, further comprising:

a sorting step that sorts the parse trees having the goodnesses of fit that satisfy preset conditions in a descending order of the goodnesses of fit, wherein the output step outputs the parse trees sorted by the sorting step as secondary structure candidates of the RNA sequence.

45. (New) The computer readable recording medium according to claim 43, further comprising:

an extraction step that extracts the RNA sequences from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived; and

a common structure matrix creation step that displays the structural topologies and the RNA sequences in a two-dimensional matrix, that gives marks to lattice parts corresponding to the RNA sequences extracted by the extraction step and the structural topologies in the two-dimensional matrix, and that thereby visualizes the structural topologies common to the RNA sequences.

46. (New) The computer readable recording medium according to claim 43, further comprising:

an RNA sequence production step that produces RNA sequences transcribed from a DNA sequence input by a user; and

a gene prediction step that predicts parts of the DNA sequence corresponding to the RNA sequences, from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived, as gene candidates,

wherein the parsing step derives the parse trees by applying the one or more grammars to the RNA sequences produced by the RNA sequence production step.

47. (New) The computer readable recording medium according to claim 43, further comprising:

a similarity calculation step that calculates a similarity among the RNA sequences based on the goodnesses of fit calculated by the goodness-of-fit calculation step.

48. (New) A computer readable recording medium storing computer program that makes a computer execute an RNA sequence analysis method, comprising:

an extraction step that extracts the RNA sequences from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived;

a goodness-of-fit matrix creation step that creates a goodness-of-fit matrix which displays the structural topologies and the RNA sequences in a two-dimensional matrix, and which displays the goodnesses of fit on lattice parts corresponding to the RNA sequences extracted by the extraction step and the structural topologies in the two-dimensional matrix; and

a common structure extraction step that sorts the structural topologies according to the goodnesses of fit for the goodness-of-fit matrix created by the goodness-of-fit matrix creation step, that parses other RNA sequences based on the grammar corresponding to an order of the sorted structural topologies, and obtains the parse trees having optimum goodnesses of fit, and that extracts the other RNA sequences corresponding to the parse trees having the goodnesses of fit that satisfy the preset conditions.